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The following supplement accompanies the article

Patterns and drivers of fish community assembly in a large marine ecosystem

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Table S1. Species list and traits of demersal fish species present in the Baltic Sea International Trawl Survey (BITS) in Quarter 1 from 2003 to 2014. The 'diet' is taken from FishBase; 'Lmean' is the mean length of the species in the survey; 'A50' and 'Fecundity' are taken from Fishbase, ICES species sheet facts and stock assessment or from the literature as stated in Ref; 'caudal' and 'body' shape are derived from FishBase pictures.

Species	Diet	Lmean	A50	Fecundity	Caudal	Body	Ref	Area
Agonus cataphractus	benthivorous	135	2	3000	rounded	elongated	[1]	Baltic Sea
Amblyraja radiata	generalist	390	5.5	50	continuous	flat	[2]	North Sea
Ammodytidae	planktivorous	179	1.5	5000	forked	elongated	[3]	North Sea
Anguilla anguilla	generalist	570	12	2000000	continuous	eellike	[4,5]	Europe
Arnoglossus laterna	generalist	120	2	50000	rounded	flat	[6]	Scotland
Buglossidium luteum	benthivorous	100	3	13400	rounded	flat	[7]	English Channel
Callionymus	benthivorous	126	2.5	5000	rounded	normal	[8]	North Sea
Chelidonichthys lucernus	generalist	266	2	100000	truncated	normal	[9]	Mediterranean
Cyclopterus lumpus	planktivorous	205	5	100000	truncated	normal	[10]	Baltic Sea
Enchelyopus cimbrius	generalist	231	3	30000	rounded	elongated	[11]	?
Eutrigla gurnardus	generalist	170	3	14347	emarginated	normal	[8]	Irish Sea
Gadus morhua	piscivorous	303	3	1000000	truncated	normal	[12]	Baltic Sea
Glyptocephalus cynoglossus	benthivorous	230	4.5	100000	rounded	flat	[13]	Gulf of Maine
Gobiidae	generalist	73	1	4000*	rounded	normal	[1]	Baltic Sea
Hippoglossoides platessoides	generalist	160	10	380000	rounded	flat	[14]	Barents Sea
Hyperoplus	planktivorous	201	2	7000	forked	elongated	[1]	North Sea
Lepidorhombus whiffiagonis	generalist	129	2	300000	rounded	flat	[15]	Ireland
Limanda limanda	benthivorous	186	2.5	150000	rounded	flat	[16]	North Sea
Lumpenus lampretaeformis	benthivorous	226	3	1000	rounded	eellike	[17]	Barents Sea
Melanogrammus aeglefinus	generalist	222	2.5	535000	emarginated	normal	[18,19]	North Sea
Merlangius merlangus	piscivorous	208	2	400000	truncated	normal	[20]	Irish Sea
Merluccius merluccius	piscivorous	252	4.4	1000000	truncated	elongated	[21,22]	Bay of Biscay
Microstomus kitt	benthivorous	223	4	200000	rounded	flat	[8]	North Sea
Mullus barbatus	benthivorous	114	1.5	10000	forked	normal	[23]	Mediterranean
Mullus surmuletus	generalist	121	1.5*	10000**	forked	normal	[23]	Mediterraneen
Myoxocephalus quadricornis	generalist	190	2**	10000***	truncated	normal	[24]	Barents Sea
Myoxocephalus scorpius	generalist	210	2	10000	rounded	normal	[24]	Barents Sea
Myxine glutinosa	benthivorous	293	3	100	continuous	eellike	[25]	Europe
Pholis gunnellus	benthivorous	176	2	100	rounded	eellike	[1]	Baltic Sea
Platichthys flesus	benthivorous	274	2	1000000	rounded	flat	[11]	Bay of Biscay
Pleuronectes platessa	benthivorous	259	2.5	552000	rounded	flat	[26]	Barents Sea
Pollachius virens	piscivorous	298	4.6	2900000	emarginated	normal	[8]	North Sea
Salmo salar	piscivorous	664	5	17000	truncated	normal	[11]	Europe
Salmo trutta	piscivorous	573	2.5	2000	truncated	normal	[11]	Europe
Scophthalmus maximus	generalist	296	3	5000000	rounded	flat	[27]	Baltic Sea
Scophthalmus rhombus	generalist	292	1.6	5000000	rounded	flat	[28,29]	Europe
Solea solea	benthivorous	240	3	300000	rounded	flat	[30]	North Sea
Squalus acanthias	piscivorous	693	30	6	emarginated	elongated	[31]	Baltic Sea
Syngnathidae	generalist	258	1	65****	rounded	eellike	[32]	Aegan Sea
Trachinus draco	generalist	215	1	57600	truncated	normal	[33,34]	Baltic Sea
Trisopterus minutus	generalist	145	1	10000	truncated	normal	[35]	Aegan Sea
Zoarces viviparus	benthivorous	227	2	100	continuous	eellike	[36]	Baltic Sea

* As *Gobius niger* ** As *Mullus barbatus* *** As *Myoxocephalus Scorpius* **** As *Syngnathus acus*

Table S2. Initial traits database and the final 6 traits selected (bold).

Trophic level
Trophic guilds (Diet)
Maximum length (Lmax)
Length at 50% maturity (L50)
Mean survey length (Lmean)
Age at 50% maturity (A50)
Life expectancy
Offspring size
Fecundity
Schooling behaviour
Caudal shape
Body shape
Barbels presence

Table S3. Spatial autocorrelation of the residuals from the gam model: Mantel test (R package vegan)

Gam Model	Mantel statistic r	P-value
SR~ Salinity	0.0063	0.45
SR~ Salinity + habitat + Oxygen	0.0268	0.29
FR ~ Salinity	0.0063	0.39
FR ~ Salinity + habitat	0.0315	0.27

Table S4. Variables and parameters of the final generalized additive models (GAMs). Sign: whether the fitted relationships are predominately positive or negative; edf: estimated degrees of freedom for the model smooth terms (edf > 1 indicates a nonlinear relationship); DEV: degree of explained variance; Significance code: *p<0.05, **p<0.01, *** p<0.001.

Metrics	Best models and individual parameters	Sign	edf	DEV (%)
Species Richness	Best model: Salinity + Oxygen + habitat			92.5
	Salinity***	+	1.91	
	Oxygen***	+	0.94	
	Habitat***	-	0.94	
	Best single-variable model: Salinity			84.7
	Salinity***	+	1.88	
Functional Richness	Best model: Salinity + habitat			63.1
	Salinity***	+	1.72	
	Habitat***	-	0.87	
	Best single-variable model: Salinity			53,8
	Salinity***	+	1.81	
Functional Evenness	Best model: Depth sd + Depth + habitat			37.1
	Depth sd ***	+	1.8	
	Depth ***	+	1	
	Habitat *	□	0.7	
	Best single-variable model:			11.5
	Temperature *	□	1.2	
Functional Divergence	Best model: Depth sd			19.9
	Depth sd**	□	1.3	

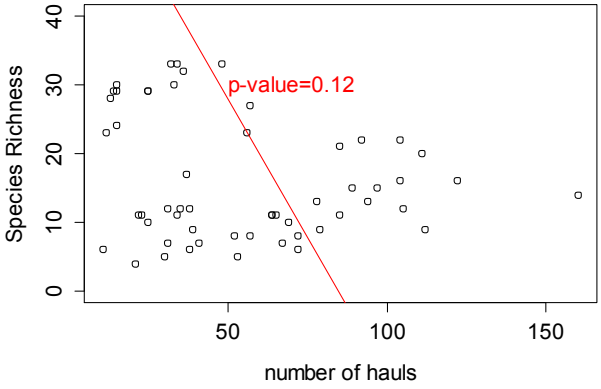

Figure S1. No influence of the sampling effort on the species richness

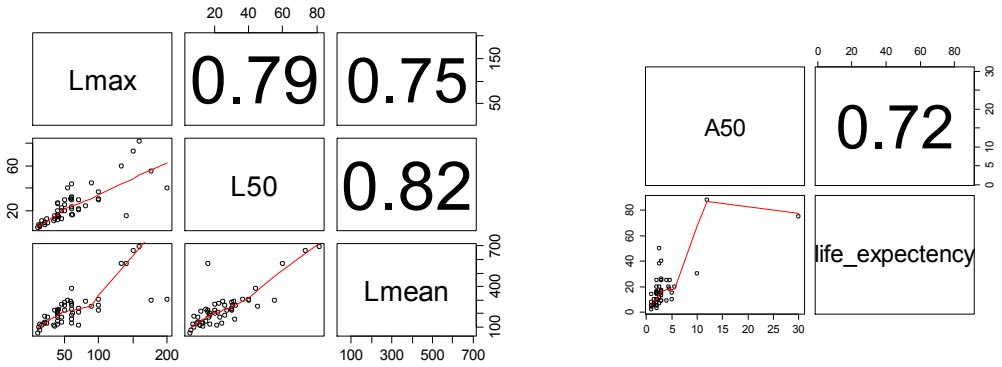

Figure S2. Correlations and Pearson coefficient between the different length metrics (left) and age metrics (right)

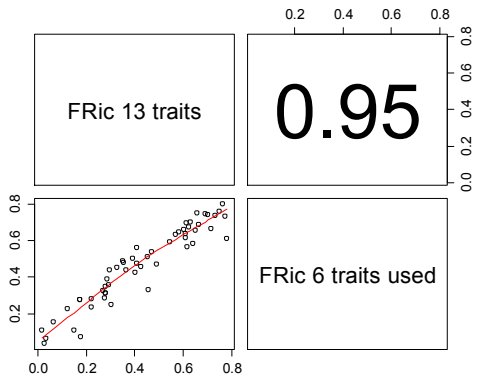

Figure S3. Influence of the traits database chosen: correlation (Pearson) between functional richness calculated with the 13 traits compared to functional richness calculated with the 6 selected traits only.

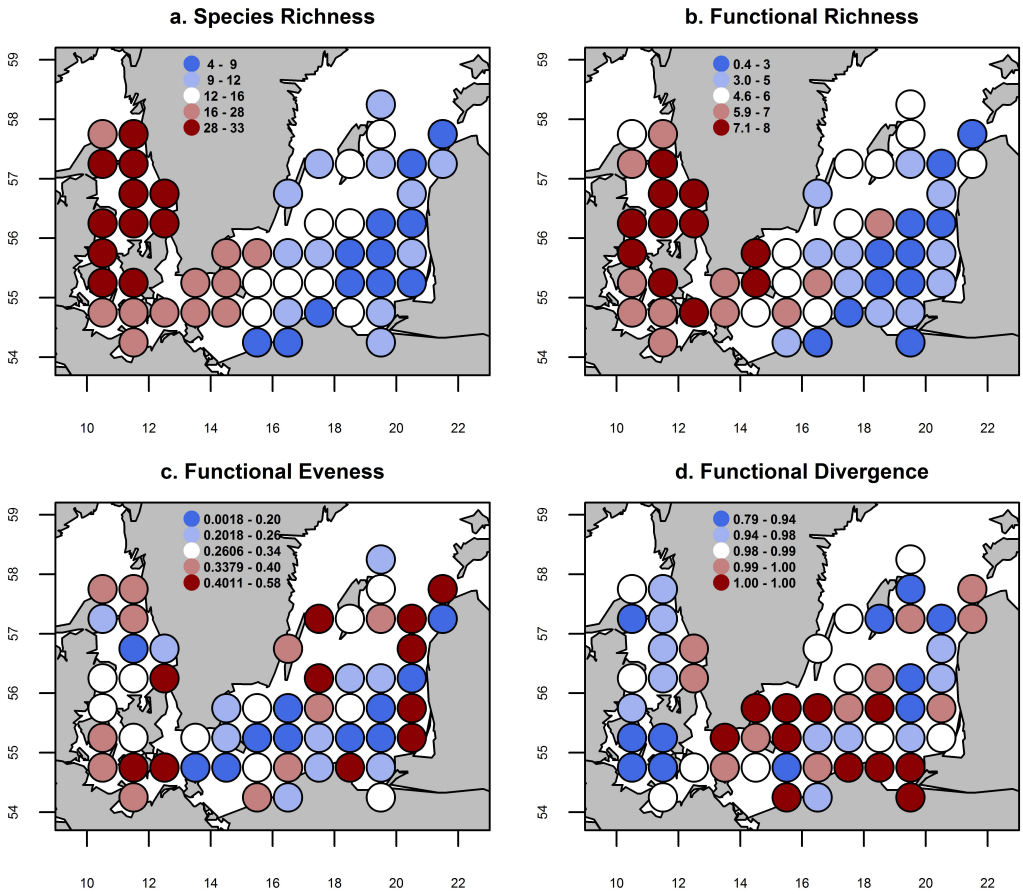

Figure S4. Species Richness and the three facets of functional diversity [37] of the Baltic Sea demersal fish communities. The values are cut in quintiles.

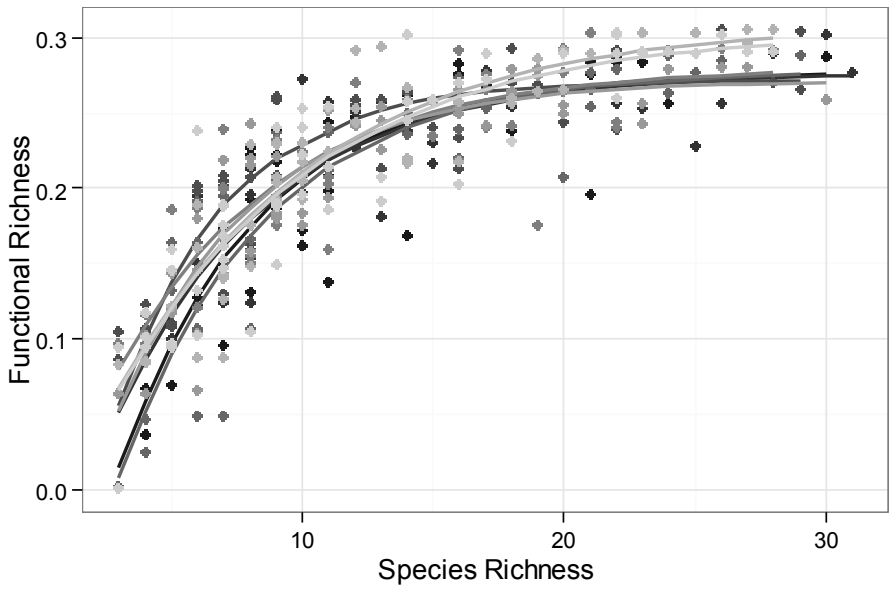

Figure S5. Temporal study of the relationship between SR and FRic. The years from 2004 to 2012 are represented using a grey scale (from dark in 2004 to light grey in 2012).

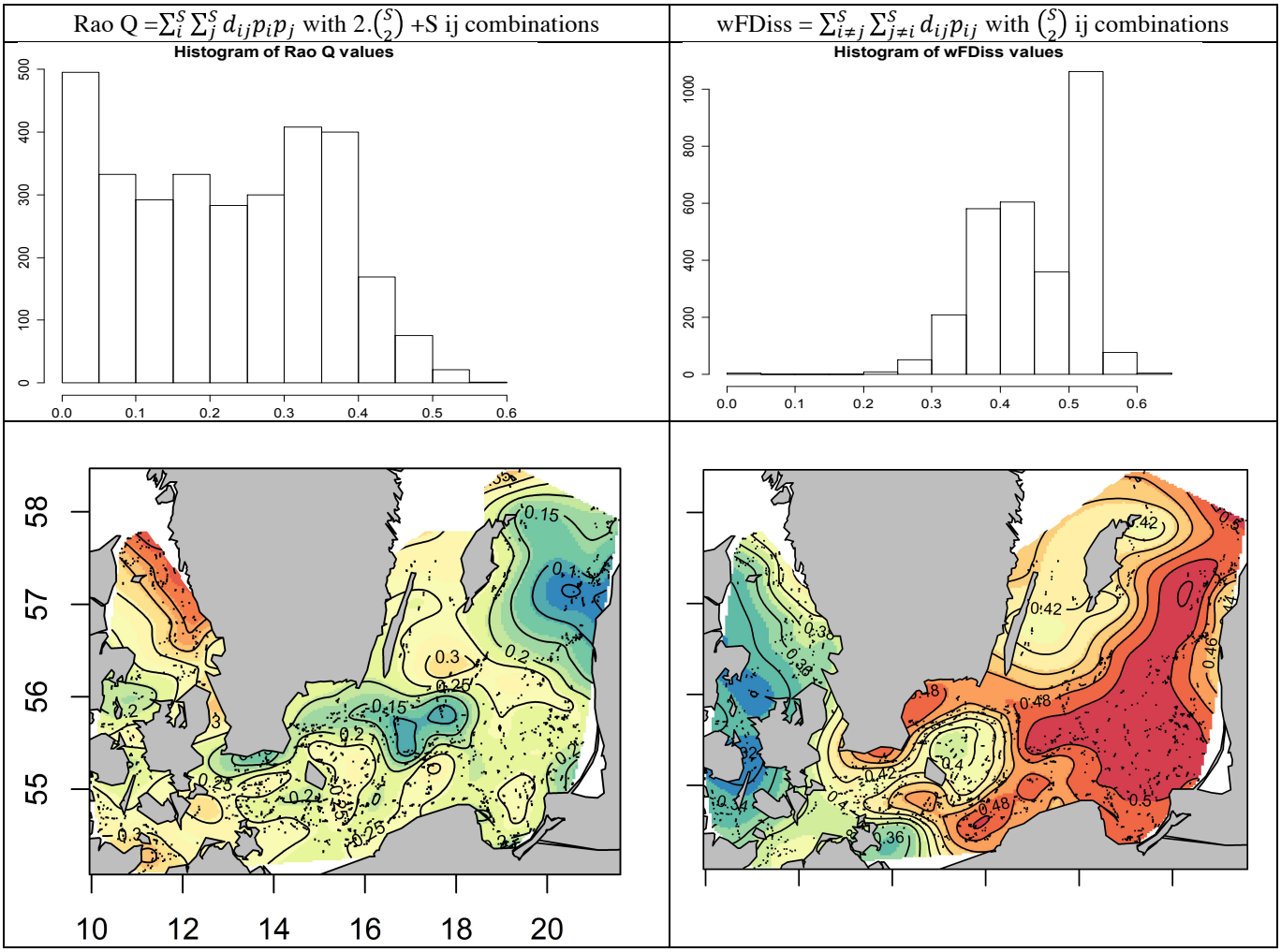

Figure S6. Rao Q versus wFDiss. Rao Q [38] represents the average functional dissimilarity, i.e. distance, of two individuals randomly selected in a community, while wFDiss represents the average functional dissimilarity of two individuals from two different species in a community. Hence, Rao Q is always lower than wFDiss as it takes into account the functional dissimilarity of two individuals from the same species (d_{ii}=0). Green colors represent lower Rao Q or wFDiss values, whilst red colors represents higher values. The black points represents the single hauls from which a smoothing function was applied (thin plate spline regression from fields package in R).

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